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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: O'Malley, Bert W.

Tsai, Ming-Jer

Ledebur, Harry C. Jr. Kittle, Joseph D. Jr.

(ii) TITLE OF INVENTION: MODIFIED STEROID HORMONES FOR GENE

HORMONES FOR GENE THERAPY AND METHODS

FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon

(B) STREET: 633 West Fifth Street

Suite 4700

(C) CITY: Los Angeles (D) STATE: California

(E) COUNTRY: U.S.A. (F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

storage

Word Perfect 5.1

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: IBM P.C. DOS 5.0

(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned

(B) FILING DATE: Herewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/479,913 (B) FILING DATE: June 7, 1995

(A) APPLICATION NUMBER: 07/939,246

(B) FILING DATE: September 2, 1992

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(viii) ATTORNEY/AGENT INFORMATION:

NAME: (A) Warburg, Richard J.

(B) REGISTRATION NUMBER: 32,327 (C) REFERENCE/DOCKET NUMBER: 222/085

(ix)

TELECOMMUNICATION INFORMATION:

(213) 489-1600 (213) 955-0440 (A) TELEPHONE: (B) TELEFAX:

(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

> LENGTH: (A) 6177 base pairs

nucleic acid (B) TYPE:

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTAGAGTCGA	CCTGCAGCCC	AAGCTCTCGA	GGGATCCTGA	GAACTTCAGG	GTGAGTTTGG	60
GGACCCTTGA	TTGTTCTTTC	TTTTTCGCTA	TTGTAAAATT	CATGTTATAT	GGAGGGGGCA	120
AAGTTTTCAG	GGTGTTGTTT	AGAATGGGAA	GATGTCCCTT	GTATCACCAT	GGACCCTCAT	180
GATAATTTTG	TTTCTTTCAC	TTTCTACTCT	GTTGACAACC	ATTGTCTCCT	CTTATTTTCT	240
TTTCATTTTC	TGTAACTTTT	TCGTTAAACT	TTAGCTTGCA	TTTGTAACGA	ATTTTTAAAT	300
TCACTTTTGT	TTATTTGTCA	GATTGTAAGT	ACTTTCTCTA	ATCACTTTTT	TTTCAAGGCA	360
ATCAGGGTAT	ATTATATTGT	ACTTCAGCAC	AGTTTTAGAG	AACAATTGTT	ATAATTAAAT	420
	AATATTTCTG				CTTATTGGTA	480
	CATCCTGGTC					540
	GAGGATAAAA					600
	CTTTTTCCTA					660
	AGAATTCACT			TCAGAAGGTG	GTGGCTGGTG	720
	CCTGGCTCAC			TCCCTCTGCC		780
	GAAGCCCCTT					840
	GTGTTGGAAT					900
	ACATCAGAAT					960
GGCTGCCATG	AACAAAGGTG				GCCCCCTGCT	1020
GTCCATTCCT			ACTTGAGGTT		TATATTTTGT	1080
TTTGTGTTAT			AAATTTTCCT			1140
	TCTCCTGACT					1200
	GCAAAAGCCT					1260
	GGCGGCCTCG					1320
	GGAACTGGGC					1380
	CTAATTGAGA					1440
	GCGCTCTTCC					1500
	GGTATCAGCT					1560
	AAAGAACATG					1620
	GGCGTTTTTC					1680
	GAGGTGGCGA					1740
	CGTGCGCTCT					1800
	GGGAAGCGTG					1860
TGTAGGTCGT			TGCACGAACC			1920
	CGGTAACTAT					1980
	CACTGGTAAC					2040
	GTGGCCTAAC					2100
	AGTTACCTTC					2160
CCGCTGGTAG	CGGTGGTTTT	TTTGTTTGCA	AGCAGCAGAT	TACGCGCAGA	AAAAAAGGAT	2220

	TCCTTTGATC					2280
	TTTGGTCATG					2340
	TTTTAAATCA					2400
AATGCTTAAT	CAGTGAGGCA	CCTATCTCAG	CGATCTGTCT	ATTTCGTTCA	TCCATAGTTG	2460
CCTGACTCCC	CGTCGTGTAG	ATAACTACGA	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG	2520
CTGCAATGAT	ACCGCGAGAC	CCACGCTCAC	CGGCTCCAGA	TTTATCAGCA	ATAAACCAGC	2580
CAGCCGGAAG	GGCCGAGCGC	AGAAGTGGTC	CTGCAACTTT	ATCCGCCTCC	ATCCAGTCTA	2640
TTAATTGTTG	CCGGGAAGCT	AGAGTAAGTA	GTTCGCCAGT	TAATAGTTTG	CGCAACGTTG	2700
TTGCCATTGC	TACAGGCATC	GTGGTGTCAC	GCTCGTCGTT	TGGTATGGCT	TCATTCAGCT	2760
CCGGTTCCCA	ACGATCAAGG	CGAGTTACAT	GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA	2820
	TCCTCCGATC					2880
	ACTGCATAAT					2940
	CTCAACCAAG					3000
GCCCGGCGTC	AATACGGGAT	AATACCGCGC	CACATAGCAG	AACTTTAAAA	GTGCTCATCA	3060
	TTCTTCGGGG					3120
	CACTCGTGCA					3180
	AAAAACAGGA					3240
	ACTCATACTC					3300
	CGGATACATA					3360
	CCGAAAAGTG					3420
	TAGGCGTATC					3480
	GAAAACCTCT					3540
	GGGAGCAGAC					3600
	ATGACCCAGT					
	TACTGAGAGT					3660
	CAGTAGTAGG					3720 3780
	ATTAATCGAC					
	TAAATGGCCC					3840
	ATGTTCCCAT					3900
						3960
	GGTAAACTGC					4020
	ACGTCAATGA					4080
	TTCCTACTTG					4140
	GGCAGTACAT					4200
	CCATTGACGT					4260
	GTAACAACTC					4320
	TAAGCAGAGC					4380
	ACCTCCATAG					4440
	CCCGCACCTC AGAATCCTTA					4500 4560
	GGGGAGCGTA					4620
	ATCTTCGCCC					
	TGATTTCTCG					4680 4740
	GCAGCAGCAG					
						4800
	ACTGTCCATG					4860
	CTACCCACAG					4920
	AGAAAGCATT					4980
	GTCTGCAACT					5040
	ATCTTCAGAA					5100
	GTATCCCACA					5160
	CCCAAGTAAA					5220
	GCTTTCTCCT					5280
	TTGTAAGCCT					5340
	CTTATCAAGT					5400
	TGAACTTTGC					5460
	AAGCTTTTCT					5520
	GAGTACCTCT					5580
	GCAGGATCAG					5640
	GAATAGGTGC					5700
	AGGCCGGTCA					5760
	TCCTCCATCC					5820
	CGATGAAGCT					5880
AAGTATTCTT	TAAAAGAGCA	GTGGAAGGAC	AGCACAATTA	CCTTTGTGCT	GGAAGAAACG	5940
	TGATAAAATT					6000
	AATGAACCTT					6060
	AGGAGTCTCA					6120
CAGCATTACC	ACAGCTCACC	CCTACCTTGG	TGTCACTGCT	GGAGGTGATT	GAACCCG	6177

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(2) INF	ORMATION FOR SEQ ID NO: 2:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
	ACGCGGCGCG CCGTCGACCT GCAGAAGCTT ACTAGTGGTA CCCCATGGAG GAATTCACGC GTTCTAGATT AATTAAGC	60 98
	ORMATION FOR SEQ ID NO: 3:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
	A TTAATCTAGA ACGCGTGAAT TCGGATCCAG ATCTCCATGG GGTACCACTA T GCAGGTCGAC GGCGCGCCGC GTTTAAAC	60 98
(2) INFO	ORMATION FOR SEQ ID NO: 4:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
GATCTCGGTC	TCCAACAGCA ACAGCAACAG CAACAGCAAC AGGGTCTTCT G	51
(2) INFO	ORMATION FOR SEQ ID NO: 5:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 51 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
GATCCAGAAG	ACCCTGTTGC TGTTGCTGTT GCTGTTGCTG TTGGAGACCG A	51

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:
(B) TYPE:

42 base pairs nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AATTCCCCGA GGCGGCAGCT GAAATCATCA CCAATCAGAT CT 42

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

18

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TATGCCTTAC CATGTGGC

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TTGGTCGACA AGATCATGCA TTATC 25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTGTCGACCC GCAGTACAGA TGAAGTTG

121 226/286 (2) INFORMATION FOR SEQ ID NO: 10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single TOPOLOGY: (D) linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: TTGGTCGACC CAGCAATAAC TTCAGACATC 30 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid STRANDEDNESS: (C) single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: CGACAGATCT GGCTCCTGAG CAAAGAGAA 29 INFORMATION FOR SEQ ID NO: 12: (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: CCAGGGATCC TCTCCTTGCT GCAA 24 (2) INFORMATION FOR SEQ ID NO: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs nucleic acid (B) TYPE: (C) STRANDEDNESS: single TOPOLOGY: linear (D) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

33

TCTAGTCGAC GATGGCTCCT GAGCAAAGAG AAG

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(2)	INFORMATION	FOR	SEO	ID	NO:	14:

- (i) SEQUENCE CHARACTERISTICS:
 - 27 base pairs nucleic acid single linear (A) LENGTH: (B) TYPE:
 - (C) STRANDEDNESS: TOPOLOGY: (D)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CCAGGGATCC TATCCTTGCT GCAACAG 27